

Seq ID NO: 7

Database : A_Geneseq_23Sep04:*
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 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2794	100.0	497	3	AA93750	Aay93750 Amino aci
2	439.5	15.7	174	6	AAE30346	Aae30346 Perna can
3	439.5	15.7	175	6	AAE30347	Aae30347 Crassostr
4	260	9.3	1529	2	AAR97985	Aar97985 CORK pota
5	217	7.8	351	2	AAR24393	Aar24393 Sequence
6	178	6.4	339	6	ADA35264	Ada35264 Acinetoba
7	173.5	6.2	244	2	AAR67409	Aar67409 Rat super
8	173.5	6.2	244	5	AAM52476	Aam52476 Superoxid
9	173.5	6.2	244	7	ADD48518	Add48518 Rat Prote
10	172.5	6.2	221	2	AAR27934	Aar27934 GAG fusio

mini work

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	178	6.4	339	4	US-09-328-352-6551	Sequence 6551, App
2	173.5	6.2	244	3	US-08-679-493A-188	Sequence 188, App
3	168	6.0	150	2	US-08-722-050-9	Sequence 9, Appli
4	168	6.0	150	4	US-09-883-985-9	Sequence 9, Appli
5	167	6.0	154	3	US-08-679-493A-211	Sequence 211, App
6	166	5.9	151	2	US-08-722-050-10	Sequence 10, Appl
7	166	5.9	151	4	US-09-883-985-10	Sequence 10, Appl
8	165.5	5.9	152	2	US-08-722-050-12	Sequence 12, Appl
9	165.5	5.9	152	4	US-09-883-985-12	Sequence 12, Appl
10	164.5	5.9	153	3	US-08-679-493A-207	Sequence 207, App
11	164	5.9	151	3	US-08-679-493A-191	Sequence 191, App
12	163.5	5.9	153	3	US-08-679-493A-201	Sequence 201, App
13	161.5	5.8	153	3	US-08-679-493A-202	Sequence 202, App
14	160.5	5.7	152	6	5171680-3	Patent No. 5171680
15	160	5.7	1099	4	US-09-881-654-4	Sequence 4, Appli
16	160	5.7	1099	4	US-10-637-323-4	Sequence 4, Appli
17	159.5	5.7	699	4	US-09-538-092-995	Sequence 995, App
18	159	5.7	166	3	US-08-679-493A-209	Sequence 209, App

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				ID	Description
		Match	Length	DB			
1	170	6.1	152	17	US-10-425-115-233754		Sequence 233754,
2	170	6.1	153	15	US-10-425-114-48136		Sequence 48136, A
3	170	6.1	153	15	US-10-425-114-52073		Sequence 52073, A
4	170	6.1	153	15	US-10-425-114-52143		Sequence 52143, A
5	170	6.1	153	15	US-10-425-114-59106		Sequence 59106, A
6	170	6.1	153	15	US-10-425-114-61368		Sequence 61368, A
7	170	6.1	153	15	US-10-425-114-62898		Sequence 62898, A
8	170	6.1	153	15	US-10-425-114-66160		Sequence 66160, A
9	170	6.1	153	15	US-10-425-114-72460		Sequence 72460, A

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	213	7.6	351	1	KGZQHL	histidine-rich gly
2	204.5	7.3	735	2	T45059	hypothetical prote
3	178	6.4	152	2	JW0084	superoxide dismuta
4	178	6.4	852	2	A34373	histidine-rich cal
5	174.5	6.2	251	2	S52859	superoxide dismuta
6	173.5	6.2	152	2	T06570	superoxide dismuta
7	173.5	6.2	244	2	A49097	superoxide dismuta
8	173	6.2	1840	2	T29091	transitin - chicke
9	168	6.0	151	2	A29077	superoxide dismuta
10	167	6.0	154	1	DSBYC	superoxide dismuta
11	164.5	5.9	154	1	DSHOCZ	superoxide dismuta
12	164	5.9	152	2	S07007	superoxide dismuta
13	163	5.8	152	2	S22508	superoxide dismuta
14	163	5.8	152	2	S72235	superoxide dismuta

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2790	99.9	517	2	Q9BKB9	Q9bkb9 perna canal
2	439.5	15.7	174	2	Q86FW9	Q86fw9 crassostrea
3	221	7.9	294	2	Q7QDP9	Q7qdp9 anopheles g
4	213	7.6	351	1	HRPX_PLALO	P04929 plasmodium
5	204.5	7.3	735	2	Q9NES7	Q9nes7 caenorhabdi
6	196.5	7.0	2245	2	Q8IAM6	Q8iam6 plasmodium
7	191	6.8	722	2	Q7YS21	Q7ys21 macaca fasc
8	178.5	6.4	726	2	Q9QZV4	Q9qzv4 mus musculu
9	178	6.4	152	1	SODC_SOYBN	Q7mlr5 glycine max
10	178	6.4	852	1	SRCH_RABIT	P16230 oryctolagus
11	177	6.3	738	2	Q9WVE4	Q9wve4 mus musculu
12	175	6.3	151	1	SODC_HALRO	P81926 halocynthia
13	174.5	6.2	251	2	Q64466	Q64466 mus musculu
14	174	6.2	152	2	Q9ZNQ4	Q9znq4 cicer ariet
15	173.5	6.2	151	1	SODC_PEA	Q02610 pisum sativ

Q9BKB9

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ID      Q9BKB9      PRELIMINARY;      PRT;      517 AA.
AC      Q9BKB9;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Pernin precursor.
OS      Perna canaliculus (greenshell mussel).
OC      Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea;
OC      Mytiloidea; Mytilidae; Perna.
OX      NCBI_TaxID=38949;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21186417; PubMed=11290459;
RA      Scotti P.D., Dearing S.C., Greenwood D.R., Newcomb R.D.;
RT      "Pernin: a novel self-aggregating haemolymph protein from the New
RT      Zealand green-lipped mussel Perna canaliculus (bivalvia: mytilidae).";
RL      Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 128:767-779(2001).
DR      EMBL; AF273766; AAK20952.1; -.
DR      HSSP; P00445; 1F1G.
DR      GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR      GO; GO:0046872; F:metal ion binding; IEA.
DR      GO; GO:0006801; P:superoxide metabolism; IEA.
DR      InterPro; IPR001424; SOD_CU_ZN.
DR      Pfam; PF00080; Sod_Cu; 3.
DR      PRINTS; PR00068; CUZNDISMTASE.
KW      Signal.
FT      SIGNAL      1      20
FT      CHAIN      21      517      pernin.
SQ      SEQUENCE      517 AA; 57222 MW; 87B8FBFFE855501E CRC64;

Query Match      99.9%; Score 2790; DB 2; Length 517;
Best Local Similarity 99.8%; Pred. No. 1.6e-198;
Matches 496; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DGEQCNDGQNKDDHHDDHHDDHHDDDDDETMHYAQCEMEPNPHMASSLHHHVHGSIEL 60
Db      21 DGEQCNDGQNKDDHHDDHHDDHHDDDDDETMHYAQCEMEPNPHMASSLHHHVHGSIEL 80

QY      61 SQKGHGAVYLELHLVGFNTSEDHDDHHHGLHLHMLGDMASAGCDSIGELYNAHPEKHADPG 120
Db      81 SQQGHGAVYLELHLVGFNTSEDHDDHHHGLHLHMLGDMASAGCDSIGELYNAHPEKHADPG 140

QY      121 DLGDLVDDDRGVVNEVHHYAWLDIDGTAPNTEALIGHSMITLQGSHTDADTPASRIACCV 180
Db      141 DLGDLVDDDRGVVNEVHHYAWLDIDGTAPNTEALIGHSMITLQGSHTDADTPASRIACCV 200

QY      181 IGHGKARPETAAALHHELEEDKTEHYAHCDVRSNTHQPKALHHHVHGTIDFKQVGYGDLE 240
Db      201 IGHGKARPETAAALHHELEEDKTEHYAHCDVRSNTHQPKALHHHVHGTIDFKQVGYGDLE 260

QY      241 VSYHLEGFNVSDDHKDLHDVQIYANGDLTSGCDNLGAKYDPHEDYHSELGDLGDIHDDD 300
Db      261 VSYHLEGFNVSDDHKDLHDVQIYANGDLTSGCDNLGAKYDPHEDYHSELGDLGDIHDDD 320

QY      301 HGVVNESHRYSWINIFGDDSVLGRSIAIHQRDHLHKSAKIACCVIGRGQSHPEIVHRAKC 360

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Db	321	HGVVNESHRYSWINIFGDDSVLGRSIAIHQRDHLHKSAKIACCVIGRGQSHPEIVHRAKC	380
Qy	361	VVRPNTESTGLHHHVSGSITFEQTPGGSTHMTADLKGFNVEDLSHHRHGVQLHEWGDMS	420
Db	381	VVRPNTESTGLHHHVSGSITFEQTPGGSTHMTADLKGFNVEDLSHHRHGVQLHEWGDMS	440
Qy	421	HGCHSLGRMYHGHDDAHDPKRPGDLGDVIDDSHGIVHSTRTFDHLNVEDLNARSLVIMQG	480
Db	441	HGCHSLGRMYHGHDDAHDPKRPGDLGDVIDDSHGIVHSTRTFDHLNVEDLNARSLVIMQG	500
Qy	481	GHEVESERVACCVIGRA	497
Db	501	GHEVESERVACCVIGRA	517

See ID no: 6

Database : EST:*

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- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Match Length DB			ID	Description
	Score	%					
1	155.8	10.4	688	6	CD649186	CD649186	AUF_104_N
2	149.4	10.0	704	6	CD648295	CD648295	AUF_102_G
3	147.8	9.9	682	6	CD648076	CD648076	AUF_101_M
4	147.8	9.9	697	6	CD647088	CD647088	AUF_107_A
5	147.8	9.9	697	6	CD647705	CD647705	AUF_108_L
6	147.8	9.9	706	6	CD649879	CD649879	CvGil0058
7	147	9.9	698	6	CD650428	CD650428	CvGil0113
8	146.2	9.8	696	6	CD648647	CD648647	AUF_103_F
9	146.2	9.8	699	6	CD648443	CD648443	AUF_102_M
10	146.2	9.8	720	6	CD648998	CD648998	AUF_104_E
11	146.2	9.8	725	6	CD649188	CD649188	AUF_104_N
12	146.2	9.8	734	6	CD648621	CD648621	AUF_103_E
13	145.4	9.8	696	6	CD648155	CD648155	AUF_101_P
14	145.4	9.8	713	6	CD649071	CD649071	AUF_104_I
15	144.6	9.7	698	6	CD648763	CD648763	AUF_103_K

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
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3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				ID	Description
No.	Score	Match	Length	DB			
1	26	1.7	766	8	BH948315	BH948315	obu82g07.
2	26	1.7	1101	9	CNS00HD3	AL073332	Drosophil
3	25	1.7	529	5	BQ118156	BQ118156	EST603732
4	25	1.7	756	6	CB942058	CB942058	AGENCOURT
5	25	1.7	946	6	CF265550	CF265550	AGENCOURT
6	23	1.5	541	1	AI724181	AI724181	RHIZ1_8_B
7	23	1.5	602	5	BW326909	BW326909	BW326909

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 4: gb_om:*
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 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1490.6	100.0	1491	6	BD268169	BD268169 Serine pr
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	3	1484.2	99.5	1700	3	AF273766	AF273766 Perna can
	4	128.4	8.6	603	3	AY256853	AY256853 Crassostr
c	5	88.4	5.9	115758	9	AC104634	AC104634 Homo sapi
	6	86	5.8	110000	2	PFMAL13_24	Continuation (25 o
c	7	74.8	5.0	164347	9	AC104805	AC104805 Homo sapi
	8	74.8	5.0	186278	9	AC079176	AC079176 Homo sapi
c	9	74	5.0	75111	5	BX276082	BX276082 Zebrafish

RESULT 1

BD268169

LOCUS BD268169 1491 bp DNA linear PAT 17-JUL-2003

DEFINITION Serine protease inhibitors.

ACCESSION BD268169

VERSION BD268169.1 GI:33077937

KEYWORDS JP 2002534063-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1491)

AUTHORS Scotti,P.D., Dearing,S.C., Greenwood,D.R. and Newcomb,R.D.

TITLE Serine protease inhibitors

JOURNAL Patent: JP 2002534063-A 1 15-OCT-2002;

THE HORTICULTURE AND FOOD RESEARCH INSTITUTE OF NEW ZEALAND LTD

COMMENT OS Shellfish

PN JP 2002534063-A/1

PD 15-OCT-2002

PF 23-DEC-1999 JP 2000591076

PR 23-DEC-1998 NZ 333568,23-JUL-1999 NZ 336906 PI

PAUL DOUGLAS SCOTTI,SALLY CAROLINE DEARING,DAVID ROGER PI
GREENWOOD,

PI RICHARD DAVID NEWCOMB

PC C12N15/09,A23L1/305,A61K38/00,A61P7/04,A61P43/00,C07K1/14, PC
C07K14/435,

PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/99// (C12N9/99,C12R1:
91),

PC C12N15/00,C12N5/00,A61K37/02

CC Serine protease inhibitors

FH Key Location/Qualifiers

FT source 1. .1491

FT /organism='Shellfish'.

FEATURES Location/Qualifiers

source 1. .1491

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 1490.6; DB 6; Length 1491;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GAYGGGGAGCAGTGTAACGATGGGCAGAACAAAGATGACCACCATGACGACCACCACGAT 60
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Db      1 GAYGGGGAGCAGTGTAACGATGGGCAGAACAAAGATGACCACCATGACGACCACCACGAT 60

QY     61 GATCACCATGACGACCATGATGATGATGATGAAACAATGCACTATGCCCAGTGTGAAATG 120
      |||
Db     61 GATCACCATGACGACCATGATGATGATGATGAAACAATGCACTATGCCCAGTGTGAAATG 120

QY    121 GAACCAAACCTCATATGGCTAGCAGCCTTACCACCATGTCCATGGCAGCATAGAGTTG 180
      |||
Db    121 GAACCAAACCTCATATGGCTAGCAGCCTTACCACCATGTCCATGGCAGCATAGAGTTG 180

QY    181 TCACAGAAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCGGATTCAACACAAGT 240
      |||

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Db 181 TCACAGAAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCGGATTCAACACAAGT 240
 Qy 241 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 300
 Qy 301 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCCAGAAAAACATGCTGACCCTGGT 360
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 Db 301 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCCAGAAAAACATGCTGACCCTGGT 360
 Qy 361 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 420
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 Db 361 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 420
 Qy 421 TGGTTGGACATTGATGGTACAGCACCAAACACCGAAGCTCTCATTGGACACTCAATGACT 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 TGGTTGGACATTGATGGTACAGCACCAAACACCGAAGCTCTCATTGGACACTCAATGACT 480
 Qy 481 ATTTTACAAGGGAGTCACACCGATGCTGATACCCCAGCCAGTAGAATCGCCTGTTGTGTT 540
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 Db 481 ATTTTACAAGGGAGTCACACCGATGCTGATACCCCAGCCAGTAGAATCGCCTGTTGTGTT 540
 Qy 541 ATTGGTCATGGAAAAGCTCGCCCAGAAACAGCAGCTGCTCTACATCACGAGCTAGAGGAA 600
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 Db 541 ATTGGTCATGGAAAAGCTCGCCCAGAAACAGCAGCTGCTCTACATCACGAGCTAGAGGAA 600
 Qy 601 GATAAAACTGAGCATTATGCCCATTTGTGACGTAAGATCTAATACACACCAACCAAAGGCT 660
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 Db 601 GATAAAACTGAGCATTATGCCCATTTGTGACGTAAGATCTAATACACACCAACCAAAGGCT 660
 Qy 661 CTTTCATCATCATGTCCACGGAACCATCGATTTCAAACAAGTTGGTTATGGTGACCTTGAA 720
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 Db 661 CTTTCATCATCATGTCCACGGAACCATCGATTTCAAACAAGTTGGTTATGGTGACCTTGAA 720
 Qy 721 GTGTCCTACCATTTAGAGGGATTTAATGTAAGTGATGACCACAAAGATCATCTCCATGAC 780
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 Qy 781 GTACAGATCTACGCCAACGGTGACCTGACCAGTGGATGTGATAACCTCGGTGCTAAATAT 840
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 Qy 841 GATCCTCATGAAGATTACCACAGTGAGTTGGGTGATCTAGGAGATATTCACGATGATGAC 900
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 Db 841 GATCCTCATGAAGATTACCACAGTGAGTTGGGTGATCTAGGAGATATTCACGATGATGAC 900
 Qy 901 CATGGCGTTGTCAATGAAAGCCACAGATATTCTTGGATCAATATCTTCGGTGATGACAGT 960
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 Db 901 CATGGCGTTGTCAATGAAAGCCACAGATATTCTTGGATCAATATCTTCGGTGATGACAGT 960
 Qy 961 GTCCTGGGACGTTCTATTGCCATTACCAAAGAGACCATCTTCATAAAAGTGCCAAAATT 1020
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 Db 961 GTCCTGGGACGTTCTATTGCCATTACCAAAGAGACCATCTTCATAAAAGTGCCAAAATT 1020
 Qy 1021 GCCTGTTGTGTCATAGGACGTGGACAGAGCCATCCAGAAATTGTTTCACAGAGCTAAATGT 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1021 GCCTGTTGTGTCATAGGACGTGGACAGAGCCATCCAGAAATTGTTTCACAGAGCTAAATGT 1080

Qy 1081 GTTGTCTAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA 1140
 |||
 Db 1081 GTTGTCTAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA 1140

Qy 1141 TTCGAACAGACCCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT 1200
 |||
 Db 1141 TTCGAACAGACCCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT 1200

Qy 1201 AGTGAGGACTTGTCTACATCATCGTCATGGTGTGCAGCTCCATGAATGGGGAGATATGTCC 1260
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 Db 1201 AGTGAGGACTTGTCTACATCATCGTCATGGTGTGCAGCTCCATGAATGGGGAGATATGTCC 1260

Qy 1261 CATGGCTGTCACTCCTTAGGCAGAATGTACCATGGTCATGATGCTCATGACCCCAA 1320
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 Db 1261 CATGGCTGTCACTCCTTAGGCAGAATGTACCATGGTCATGATGCTCATGACCCCAA 1320

Qy 1321 AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTTCACTTAGA 1380
 |||
 Db 1321 AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTTCACTTAGA 1380

Qy 1381 ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC 1440
 |||
 Db 1381 ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC 1440

Qy 1441 GGACATGAGGTCGAGAGTGAGAGGGTTGCTTGCTGTGTTATAGGACGGGCA 1491
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 Db 1441 GGACATGAGGTCGAGAGTGAGAGGGTTGCTTGCTGTGTTATAGGACGGGCA 1491

RESULT 2

BD268170

LOCUS BD268170 1611 bp DNA linear PAT 17-JUL-2003

DEFINITION Serine protease inhibitors.

ACCESSION BD268170

VERSION BD268170.1 GI:33077938

KEYWORDS JP 2002534063-A/2.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1611)

AUTHORS Scotti,P.D., Dearing,S.C., Greenwood,D.R. and Newcomb,R.D.

TITLE Serine protease inhibitors

JOURNAL Patent: JP 2002534063-A 2 15-OCT-2002;

THE HORTICULTURE AND FOOD RESEARCH INSTITUTE OF NEW ZEALAND LTD

COMMENT OS Shellfish

PN JP 2002534063-A/2

PD 15-OCT-2002

PF 23-DEC-1999 JP 2000591076

PR 23-DEC-1998 NZ 333568,23-JUL-1999 NZ 336906 PI

PAUL DOUGLAS SCOTTI,SALLY CAROLINE DEARING,DAVID ROGER PI

GREENWOOD,

PI RICHARD DAVID NEWCOMB

PC C12N15/09,A23L1/305,A61K38/00,A61P7/04,A61P43/00,C07K1/14, PC
 C07K14/435,

PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/99// (C12N9/99,C12R1:

PC 91),

PC C12N15/00,C12N5/00,A61K37/02
CC Serine protease inhibitors
FH Key Location/Qualifiers
FT source 1. .1672
FT /organism='Shellfish'.

FEATURES
source Location/Qualifiers
1. .1611
/organism="unidentified"
/mol_type="genomic DNA"
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ORIGIN

Query Match 100.0%; Score 1490.6; DB 6; Length 1611;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GAYGGGGAGCAGTGTAAACGATGGGCAGAACAAAGATGACCACCATGACGACCACCACCGAT 60

Qy     61 GATCACCATGACGACCATGATGATGATGAAACAATGCACTATGCCAGTGTGAAATG 120
      |||
Db     61 GATCACCATGACGACCATGATGATGATGATGAAACAATGCACTATGCCAGTGTGAAATG 120

Qy    121 GAACCAAACCTCATATGGCTAGCAGCCTTCACCACCATGTCCATGGCAGCATAGAGTTG 180
      |||
Db    121 GAACCAAACCTCATATGGCTAGCAGCCTTCACCACCATGTCCATGGCAGCATAGAGTTG 180

Qy    181 TCACAGAAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCGGATTCAACACAAGT 240
      |||
Db    181 TCACAGAAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCGGATTCAACACAAGT 240

Qy    241 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 300
      |||
Db    241 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 300

Qy    301 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCAGAAAAACATGCTGACCCTGGT 360
      |||
Db    301 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCAGAAAAACATGCTGACCCTGGT 360

Qy    361 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 420
      |||
Db    361 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 420

Qy    421 TGGTTGGACATTGATGGTACAGCACCAAACACCGAAGCTCTCATTGGGACTCAATGACT 480
      |||
Db    421 TGGTTGGACATTGATGGTACAGCACCAAACACCGAAGCTCTCATTGGGACTCAATGACT 480

Qy    481 ATTTTACAAGGGAGTCACACCGATGCTGATACCCAGCCAGTAGAATCGCCTGTTGTGTT 540
      |||
Db    481 ATTTTACAAGGGAGTCACACCGATGCTGATACCCAGCCAGTAGAATCGCCTGTTGTGTT 540

Qy    541 ATTGGTCATGGAAAAGCTCGCCCAGAAACAGCAGCTGCTCTACATCACGAGCTAGAGGAA 600
      |||
Db    541 ATTGGTCATGGAAAAGCTCGCCCAGAAACAGCAGCTGCTCTACATCACGAGCTAGAGGAA 600

Qy    601 GATAAACTGAGCATTATGCCCATTTGTGACGTAAGATCTAATACACCAACCAAAGGCT 660
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Qy	721		GTGTCCTACCATTTTAGAGGGATTTAATGTAAGTGATGACCACAAAGATCATCTCCATGAC	780
Db	721		GTGTCCTACCATTTTAGAGGGATTTAATGTAAGTGATGACCACAAAGATCATCTCCATGAC	780
Qy	781		GTACAGATCTACGCCAACGGTGACCTGACCAGTGGATGTGATAACCTCGGTGCTAAATAT	840
Db	781		GTACAGATCTACGCCAACGGTGACCTGACCAGTGGATGTGATAACCTCGGTGCTAAATAT	840
Qy	841		GATCCTCATGAAGATTACCACAGTCAGTTGGGTGATCTAGGAGATATTCACGATGATGAC	900
Db	841		GATCCTCATGAAGATTACCACAGTCAGTTGGGTGATCTAGGAGATATTCACGATGATGAC	900
Qy	901		CATGGCGTTGTCAATGAAAGCCACAGATATTCCTGGATCAATATCTTCGGTGATGACAGT	960
Db	901		CATGGCGTTGTCAATGAAAGCCACAGATATTCCTGGATCAATATCTTCGGTGATGACAGT	960
Qy	961		GTCCTGGGACGTTCTATTGCCATTACCAAAGAGACCATCTTCATAAAAGTGCCAAAATT	1020
Db	961		GTCCTGGGACGTTCTATTGCCATTACCAAAGAGACCATCTTCATAAAAGTGCCAAAATT	1020
Qy	1021		GCCTGTTGTGTCATAGGACGTGGACAGAGCCATCCAGAAATTGTTTCACAGAGCTAAATGT	1080
Db	1021		GCCTGTTGTGTCATAGGACGTGGACAGAGCCATCCAGAAATTGTTTCACAGAGCTAAATGT	1080
Qy	1081		GTTGTCAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA	1140
Db	1081		GTTGTCAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA	1140
Qy	1141		TTCGAACAGACCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT	1200
Db	1141		TTCGAACAGACCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT	1200
Qy	1201		AGTGAGGACTTGTCACATCATCGTCATGGTGTGCAGCTCCATGAATGGGGAGATATGTCC	1260
Db	1201		AGTGAGGACTTGTCACATCATCGTCATGGTGTGCAGCTCCATGAATGGGGAGATATGTCC	1260
Qy	1261		CATGGCTGTCACTCCTTAGGCAGAATGTACCATGGTCATGATGATGCTCATGACCCCAA	1320
Db	1261		CATGGCTGTCACTCCTTAGGCAGAATGTACCATGGTCATGATGATGCTCATGACCCCAA	1320
Qy	1321		AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTCATTCAACTAGA	1380
Db	1321		AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTCATTCAACTAGA	1380
Qy	1381		ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC	1440
Db	1381		ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC	1440
Qy	1441		GGACATGAGGTCGAGAGTGAGAGGGTTGCTTGCTGTGTTATAGGACGGGCA	1491

polyA_signal 1650..1655
ORIGIN

Query Match 99.5%; Score 1484.2; DB 3; Length 1700;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1486; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 GAYGGGGAGCAGTGTAAACGATGGGCAGAACAAAGATGACCACCATGACGACCACCACGAT 60
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Db     94 GATGGCGAACAGTGTAAATGATGGGCAGAACAAAGATGACCACCATGACGACCACCACGAT 153

Qy     61 GATCACCATGACGACCATGATGATGATGATGAAACAATGCACTATGCCCAGTGTGAAATG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    154 GATCACCATGACGACCATGATGATGATGATGAAACAATGCACTATGCCCAGTGTGAAATG 213

Qy    121 GAACCAAACCCTCATATGGCTAGCAGCCTTCACCACCATGTCCATGGCAGCATAGAGTTG 180
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Db    214 GAACCAAACCCTCATATGGCTAGCAGCCTTCACCACCATGTCCATGGCAGCATAGAGTTG 273

Qy    181 TCACAGAAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCTGGATTCAACACAAGT 240
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Db    274 TCACAGCAGGGTCATGGAGCTGTTTATCTAGAACTTCATCTTGTCTGGATTCAACACAAGT 333

Qy    241 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 300
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Db    334 GAAGACCATGACGACCACCATCATGGACTTCATCTGCACATGCTTGGTGACATGTCAGCA 393

Qy    301 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCAGAAAAACATGCTGACCCTGGT 360
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Db    394 GGTGTGATTCTATTGGCGAACTGTACAATGCTCACCAGAAAAACATGCTGACCCTGGT 453

Qy    361 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    454 GACCTCGGTGACCTGGTTGACGATGATAGGGGCGTGGTTAATGAAGTTCATCATTATGCT 513

Qy    421 TGGTTGGACATTGATGGTACAGCACCAAACACCGAAGCTCTCATTGGACACTCAATGACT 480
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Qy    481 ATTTTACAAGGGAGTCACACCGATGCTGATACCCCAGCCAGTAGAATCGCCTGTTGTGTT 540
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Qy    541 ATTGGTCATGGAAAAGCTCGCCCAGAAACAGCAGCTGCTCTACATCACGAGCTAGAGGAA 600
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Qy    601 GATAAAACTGAGCATTATGCCCATTTGTGACGTAAGATCTAATACACACCAACCAAAGGCT 660
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Db    694 GATAAAACTGAGCATTATGCCCATTTGTGACGTAAGATCTAATACACACCAACCAAAGGCT 753

Qy    661 CTTTCATCATCATGTCCACGGAACCATCGATTTCAAACAAGTTGGTTATGGTGACCTTGAA 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    754 CTTTCATCATCATGTCCACGGAACCATCGATTTCAAACAAGTTGGTTATGGTGACCTTGAA 813

Qy    721 GTGTCCTACCATTTAGAGGGATTTAATGTAAGTGATGACCACAAAGATCATCTCCATGAC 780
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Db 814 GTGTCCTACCATTTAGAGGGATTTAATGTAAGTGATGACCACAAAGATCATCTCCATGAC 873
 Qy 781 GTACAGATCTACGCCAACGGTGACCTGACCAGTGGATGTGATAACCTCGGTGCTAAATAT 840
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 Db 874 GTACAGATCTACGCCAACGGTGACCTGACCAGTGGATGTGATAACCTCGGTGCTAAATAT 933
 Qy 841 GATCCTCATGAAGATTACCACAGTGAGTTGGGTGATCTAGGAGATATTCACGATGATGAC 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 934 GATCCTCATGAAGATTACCACAGTGAGTTGGGTGATCTAGGAGATATTCACGATGATGAC 993
 Qy 901 CATGGCGTTGTCAATGAAAGCCACAGATATTCTGGATCAATATCTTCGGTGATGACAGT 960
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 Db 994 CATGGCGTTGTCAATGAAAGCCACAGATATTCTGGATCAATATCTTCGGTGATGACAGT 1053
 Qy 961 GTCCTGGGACGTTCTATTGCCATTACCAAAGAGACCATCTTCATAAAAGTGCCAAAATT 1020
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 Qy 1081 GTTGTCAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA 1140
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 Db 1174 GTTGTCAGACCTAATACAGAATCTACTGGTTTACATCACCATGTCTCTGGTTCTATAACA 1233
 Qy 1141 TTCGAACAGACCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT 1200
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 Db 1234 TTCGAACAGACCCCTGGAGGATCAACACATATGACGGCTGATCTCAAAGGATTTAACGTT 1293
 Qy 1201 AGTGAGGACTTGTCACATCATCGTCATGGTGTGCAGCTCCATGAATGGGGAGATATGTCC 1260
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 Qy 1261 CATGGCTGTCACTCCTTAGGCAGAATGTACCATGGTCATGATGATGCTCATGACCCCCAAA 1320
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 Qy 1321 AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTCATTCAACTAGA 1380
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 Db 1414 AGACCTGGTGACCTTGGTGATGTTATAGATGATTCCCATGGCATCGTTCATTCAACTAGA 1473
 Qy 1381 ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC 1440
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 Db 1474 ACCTTTGATCATCTTAATGTTGAAGATCTTAACGCACGTTCCCTTGTGATTATGCAGGGC 1533
 Qy 1441 GGACATGAGGTCGAGAGTGAGAGGGTTGCTTGCTGTGTTATAGGACGGGCA 1491
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- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
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- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1490.6	100.0	1491	3	AAA47150	Aaa47150 DNA encod
2	1490.6	100.0	1611	3	AAA47151	Aaa47151 DNA encod
3	128.4	8.6	606	8	AAD48291	Aad48291 Crassostr
4	56.8	3.8	1083	5	AAS76745	Aas76745 DNA encod
5	54.4	3.6	2000	8	ADA71938	Ada71938 Rice gene
6	52.8	3.5	110000	12	ADO34927_1	Continuation (2 of
7	52.6	3.5	583	4	AAI23356	Aai23356 Probe #13
8	52.6	3.5	583	4	ABA68463	Aba68463 Human foe
9	52.6	3.5	583	4	AAI48680	Aai48680 Probe #17
10	52.6	3.5	583	4	ABA50512	Aba50512 Human bre

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result							
No.	Score	Match	Length	DB	ID	Description	
1	54.4	3.6	480	4	US-09-248-796A-6301	Sequence 6301, Ap	
2	51.2	3.4	291	4	US-09-248-796A-6300	Sequence 6300, Ap	
3	46.4	3.1	549	4	US-09-248-796A-3913	Sequence 3913, Ap	
c 4	44.8	3.0	5340	4	US-09-627-122-21	Sequence 21, Appl	
5	42.4	2.8	2518	3	US-09-433-699-3	Sequence 3, Appli	
6	42.4	2.8	10304	4	US-09-627-465B-1	Sequence 1, Appli	
7	42	2.8	496	1	US-08-263-413-23	Sequence 23, Appl	
8	42	2.8	500	1	US-08-263-413-22	Sequence 22, Appl	
9	42	2.8	675	1	US-07-807-043B-2	Sequence 2, Appli	
10	42	2.8	675	1	US-08-299-849B-2	Sequence 2, Appli	
11	42	2.8	675	2	US-08-142-368A-2	Sequence 2, Appli	
12	42	2.8	675	3	US-08-967-727-2	Sequence 2, Appli	
13	42	2.8	675	3	US-08-037-230D-2	Sequence 2, Appli	
14	42	2.8	675	4	US-09-583-850-2	Sequence 2, Appli	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	52.6	3.5	583	9	US-09-864-761-20772	Sequence 20772, A
2	52.6	3.5	1959	9	US-09-864-761-4012	Sequence 4012, Ap
c 3	49.2	3.3	327	9	US-09-864-761-28059	Sequence 28059, A
4	49	3.3	676	17	US-10-437-963-44631	Sequence 44631, A
c 5	48.2	3.2	744802	15	US-10-292-798-1369	Sequence 1369, Ap
6	47.8	3.2	1168	15	US-10-017-161-2179	Sequence 2179, Ap
7	47.8	3.2	1168	15	US-10-292-798-1825	Sequence 1825, Ap
8	47	3.2	1631	15	US-10-369-493-36458	Sequence 36458, A
9	46.8	3.1	728	17	US-10-767-795-5840	Sequence 5840, Ap
10	46.6	3.1	717	18	US-10-425-115-15020	Sequence 15020, A
c 11	46.2	3.1	456	9	US-09-864-761-11468	Sequence 11468, A
12	45.8	3.1	493	17	US-10-767-701-31233	Sequence 31233, A
c 13	45.8	3.1	785	15	US-10-029-386-22627	Sequence 22627, A
c 14	45	3.0	506	15	US-10-029-386-20619	Sequence 20619, A
c 15	44.8	3.0	58985	10	US-09-901-152-3	Sequence 3, Appli
c 16	44.8	3.0	143601	10	US-09-855-824-3	Sequence 3, Appli
17	44.4	3.0	1028	18	US-10-739-930-4488	Sequence 4488, Ap
18	44.2	3.0	574	9	US-09-864-761-228	Sequence 228, App
19	44.2	3.0	669	9	US-09-864-761-17051	Sequence 17051, A
20	44.2	3.0	926	18	US-10-425-115-54567	Sequence 54567, A